

A little tour of assembly methods Hands-on session

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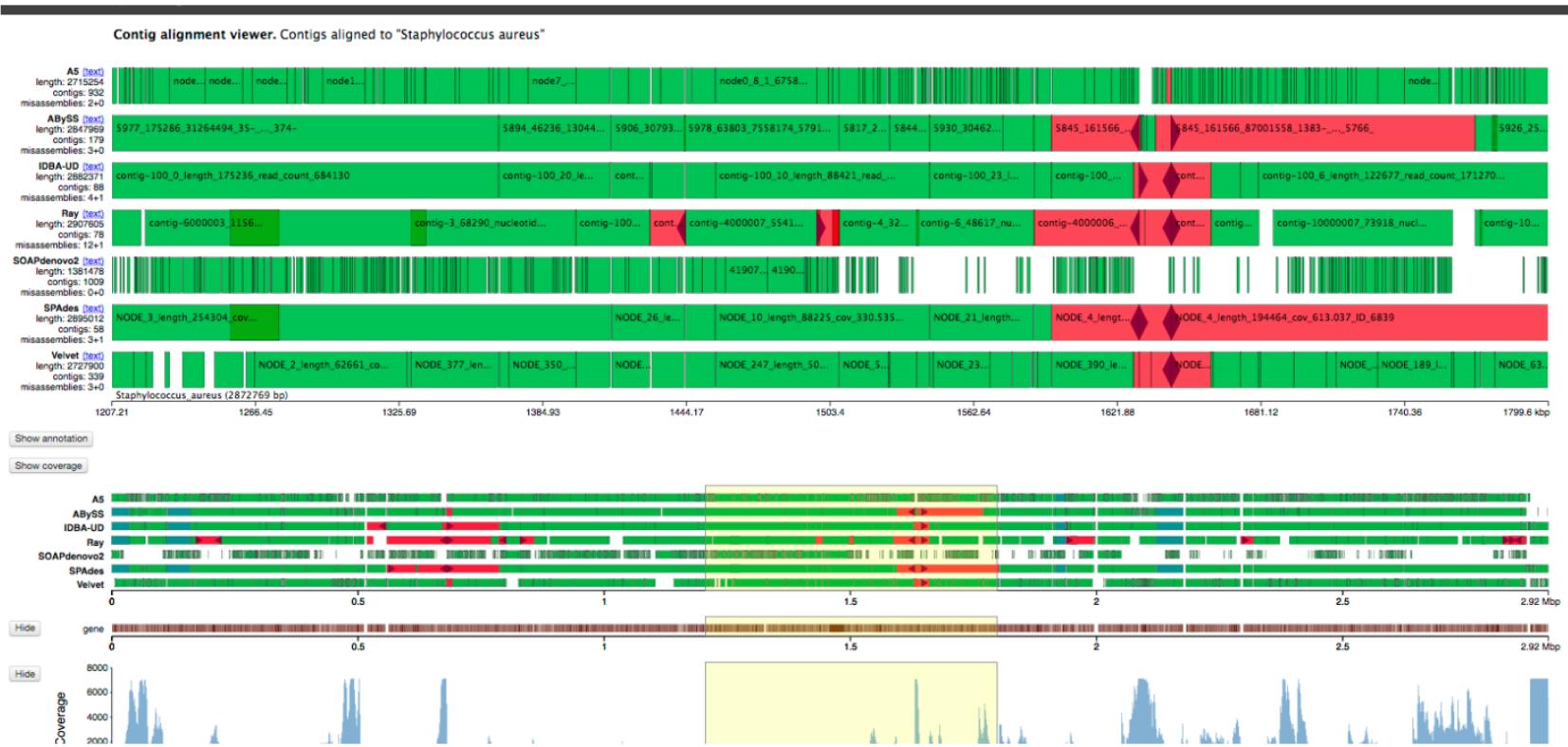
(iii)



- **Evaluate assembly according to a reference**

Contigs can be mapped and compared to a reference/closely related genome

• Evaluate assembly according to a reference (ii)



- Evaluate assembly according to a reference (iii)

From <https://quast.bioinf.spbau.ru/manual.html>

• Assembly statistics

Total aligned length	4 776 214	4 568 317	4 553 809	4 550 150
NGA50	69 801	122 647	133 309	112 446
LGA50	21	14	12	14

Misassemblies

# misassemblies	4	0	0	4
Misassembled contigs length	231 767	0	0	435 515

Per base quality

# mismatches per 100 kbp	2.09	2.69	1.03	3.19
# indels per 100 kbp	0.57	1.31	0.29	1.98
# N's per 100 kbp	24.59	0	17.55	94.19

Statistics without reference

# contigs	176	95	92	90
Largest contig	248 481	235 933	285 196	264 944
Total length	4 777 853	4 571 292	4 557 363	4 552 266
Total length (>= 1000 bp)	4 757 929	4 562 458	4 548 710	4 544 453
Total length (>= 10000 bp)	4 562 801	4 478 614	4 466 223	4 475 223
Total length (>= 50000 bp)	3 248 113	3 833 793	3 812 315	3 817 904

BUSCO completeness

- **Assembly statistics (ii)**

From <http://cab.cc.spbu.ru/quast/>

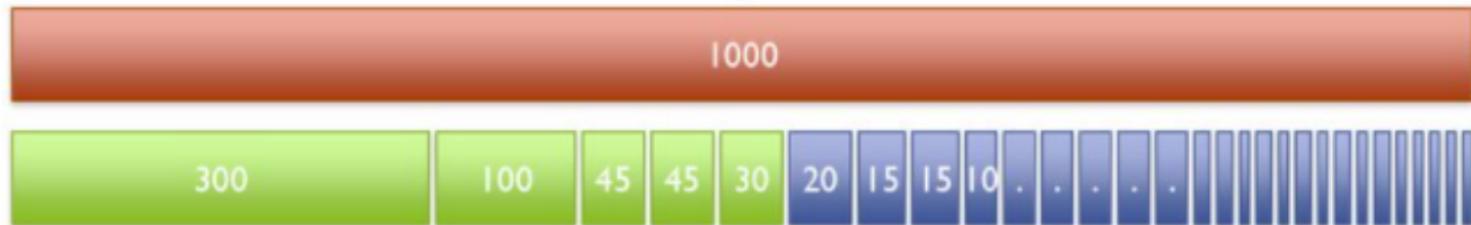
- Assembly continuity

N50

body

Example: 1 Mbp genome

50%



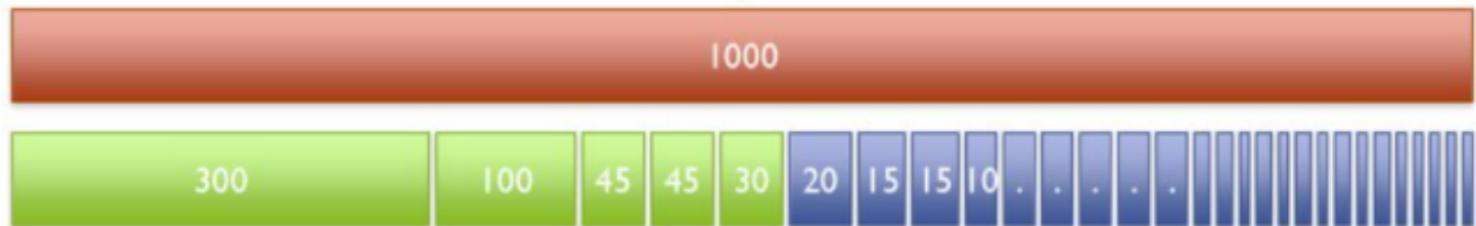
- Assembly continuity

N50

body

Example: 1 Mbp genome

50%



- **Assembly continuity**

N50

body

N75

body

NGA50

body

- Misassemblies

Contig



Reference



Relocation



Inversion



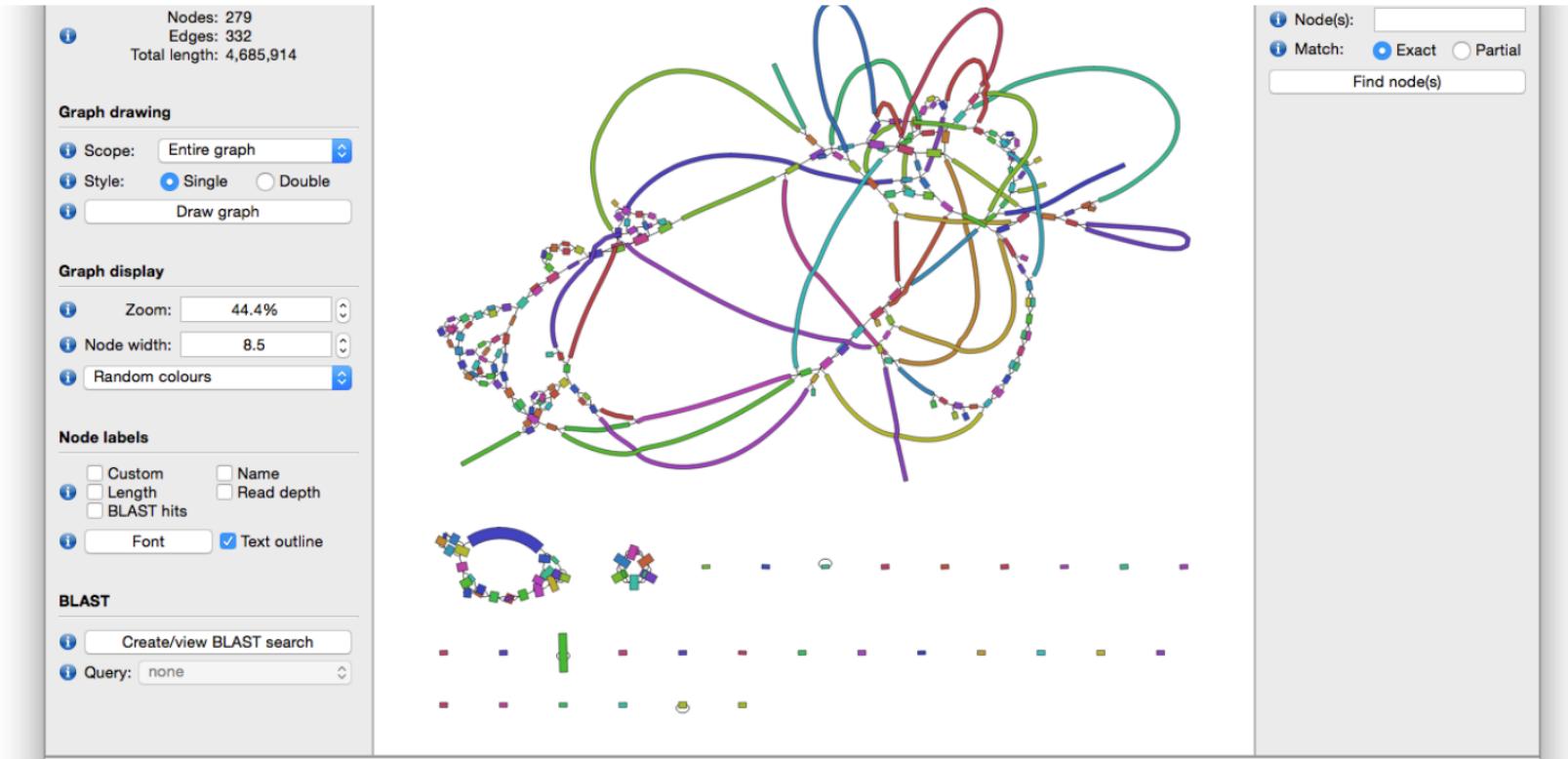
Translocation



- **Visualize assembly**

Bandage tool can visualize assembly graphs (GFA)

- Visualize assembly (ii)

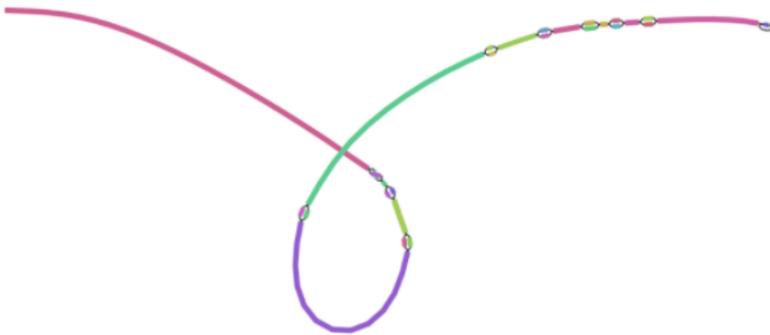


- **Visualize assembly (iii)**

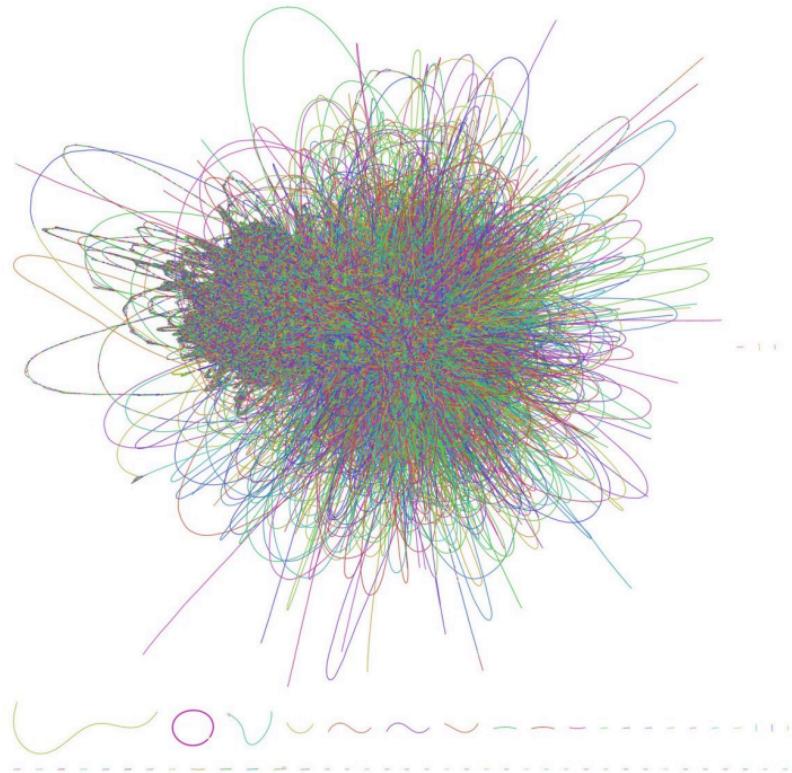
From <https://rwick.github.io/Bandage>

- **Visualize assembly**

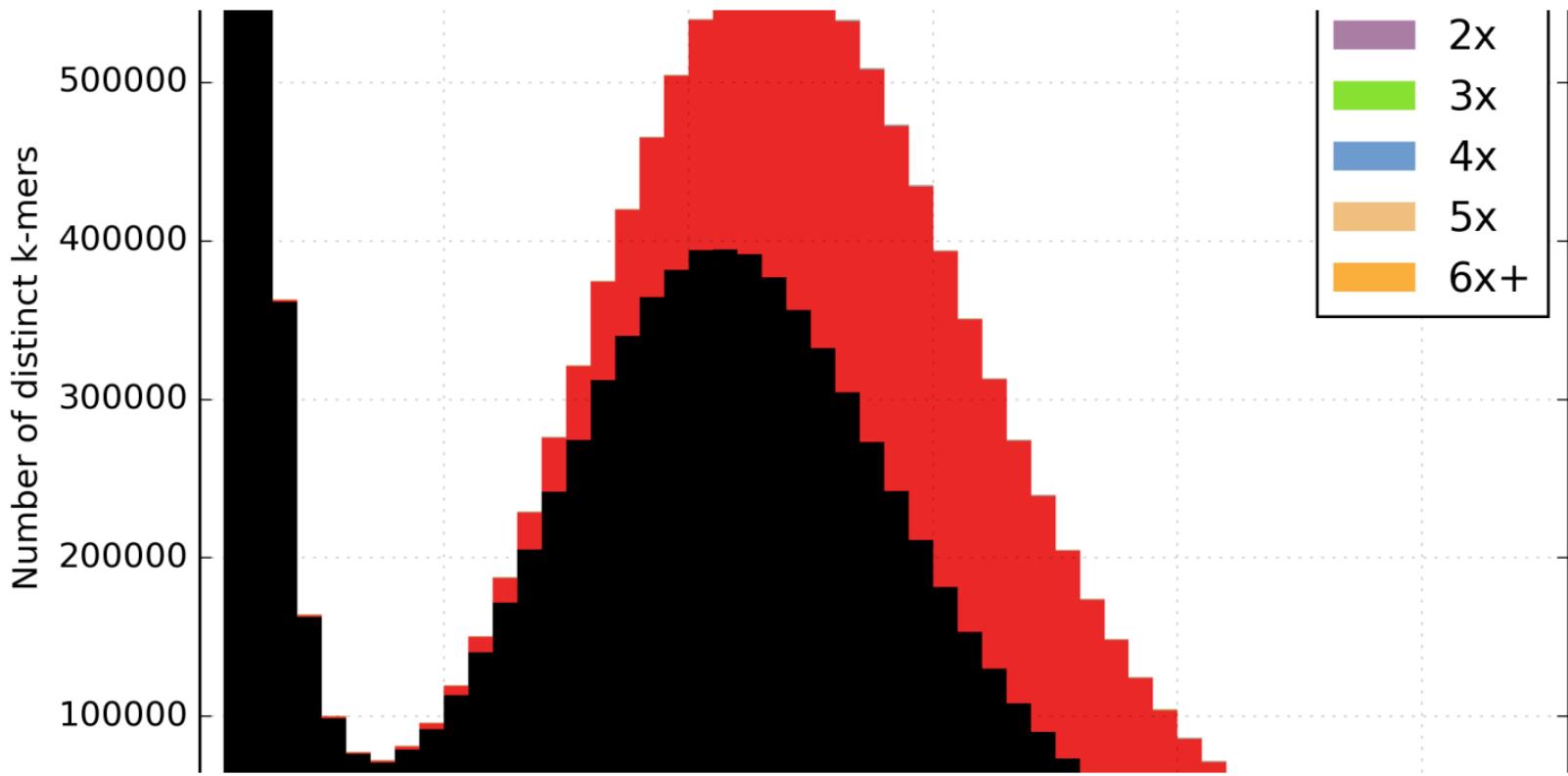
Bandage tool can visualize assembly graphs (GFA)



- Visualize assembly (ii)



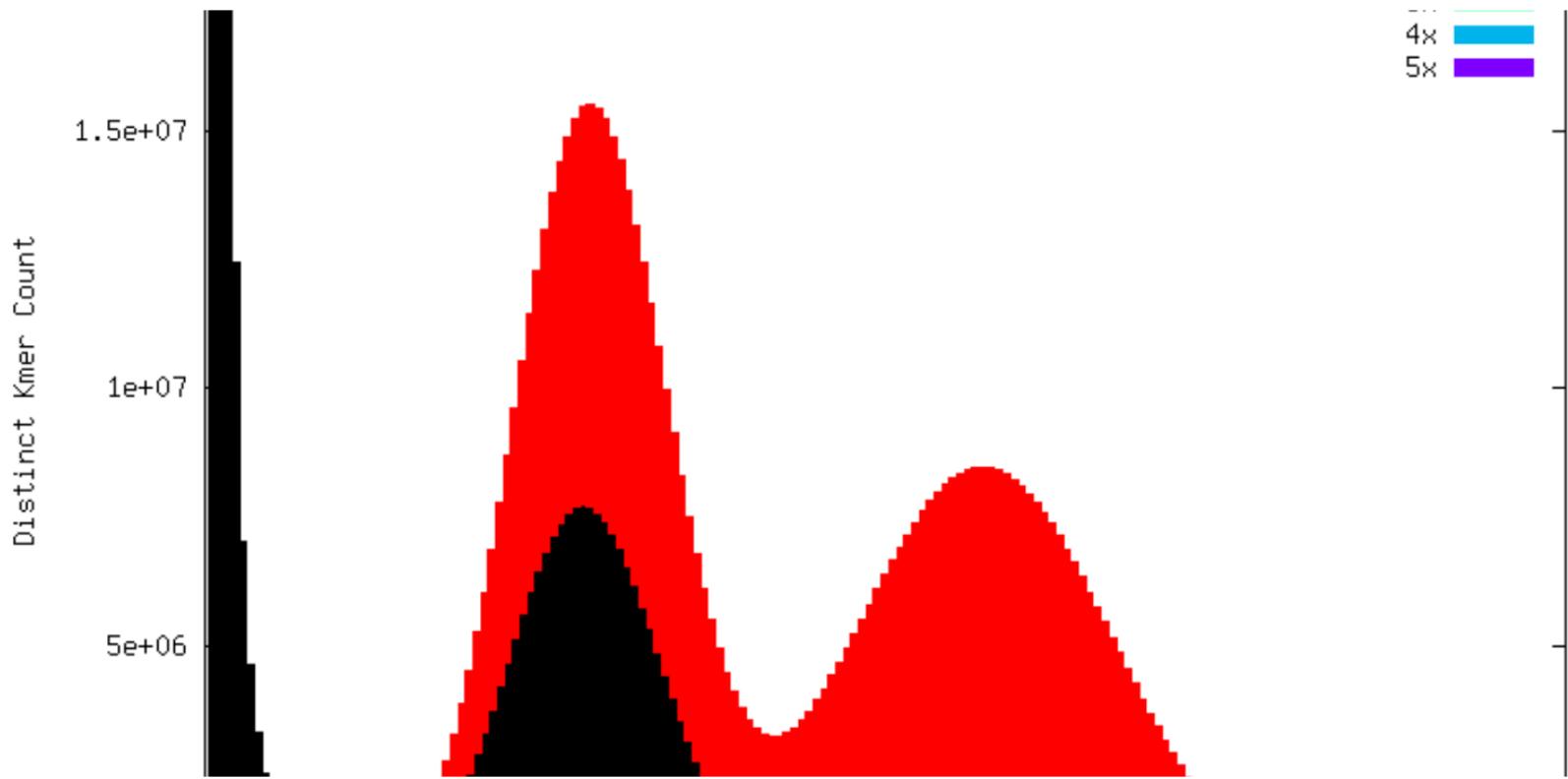
- *K*-mer spectrum visualization with KAT



- ***K*-mer spectrum visualization with KAT (ii)**

From <https://kat.readthedocs.io/en/latest/>

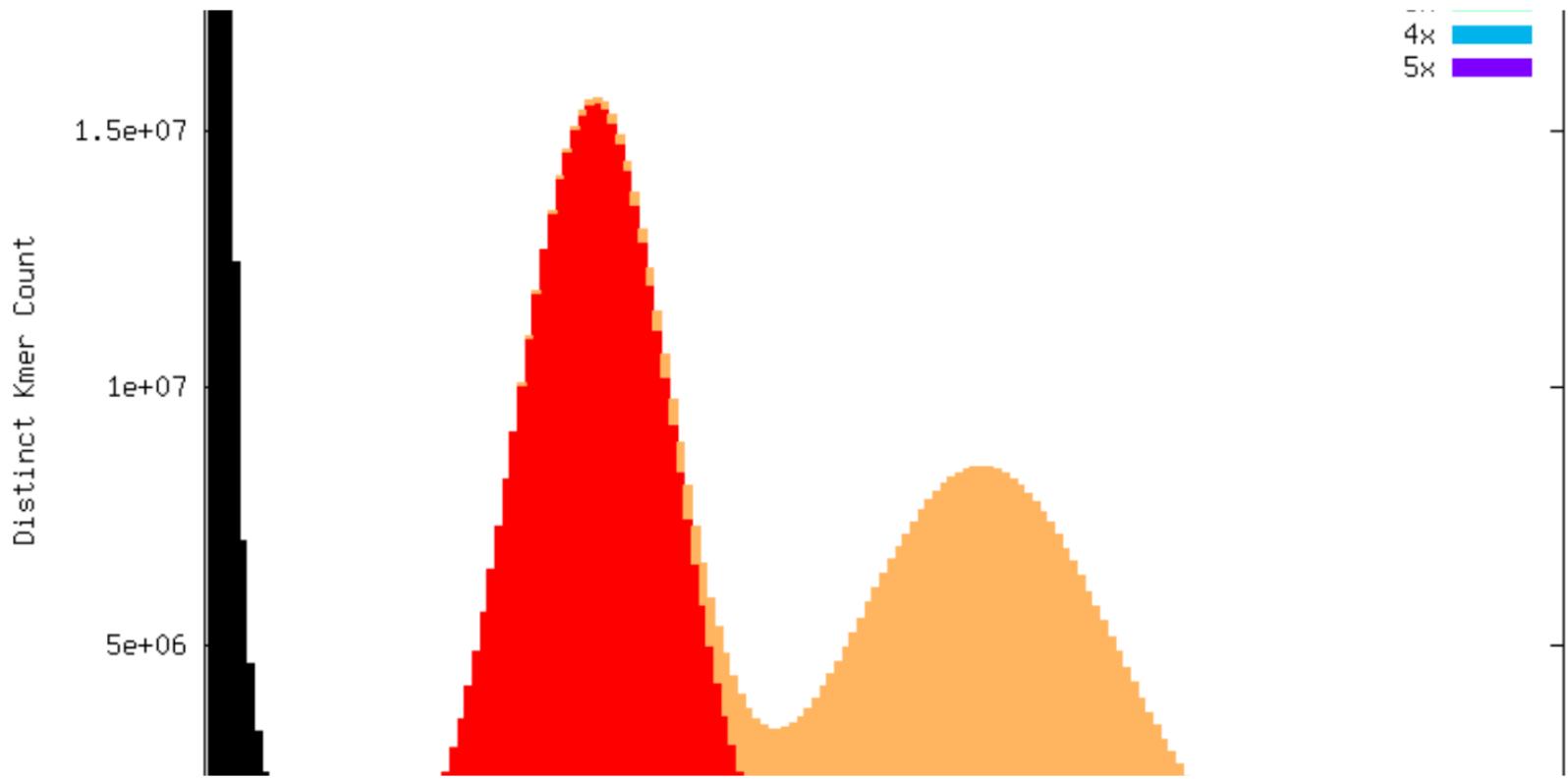
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- ***K*-mer spectrum visualization with KAT (ii)**

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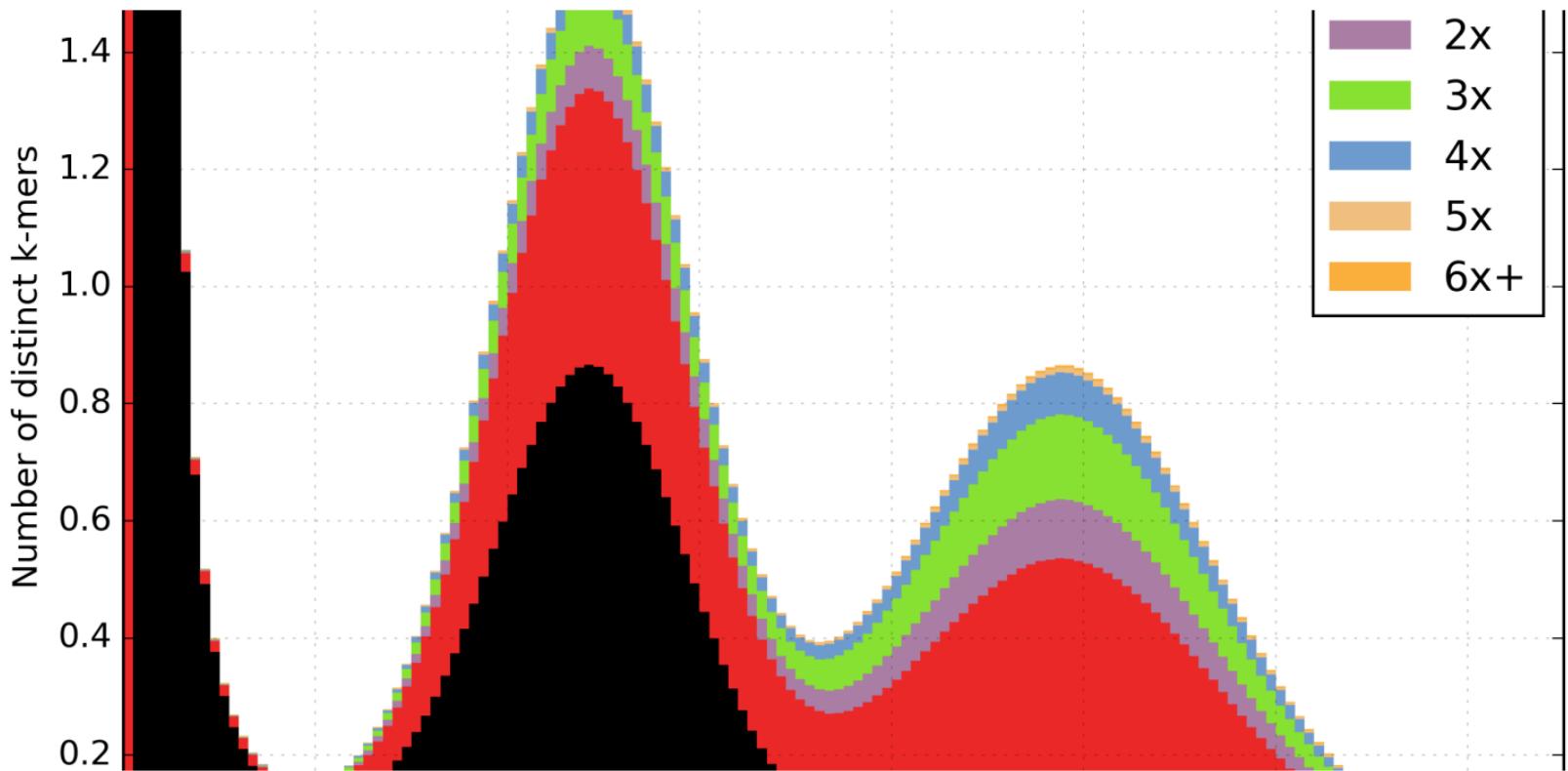
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- ***K*-mer spectrum visualization with KAT (ii)**

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- **K-mer spectrum visualization with KAT**



- ***K*-mer spectrum visualization with KAT (ii)**

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